

SEQUENCE LISTING

<110> Hayward, Nicholas K.
Weber, Gunther
Grimmond, Sean
Nordenskjold, Magnus
Larsson, Catharina

<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
SAME

<130> DAVIES

<140> 08/765,588

<141> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 649

<212> DNA

<213> Nucleotide Sequence of VEGF165

<220>

<221> CDS

<222> (17)..(589)

<400> 1

tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt 52

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu
1					5				10		

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100

Ala	Leu	Leu	Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro
	15						20					25			

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met	Ala	Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met
	30					35					40				

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp	Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp
45					50					55				60	

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser
			65					70						75	

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg	292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg	340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag	388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa	436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa	484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln	
145 150 155	
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc	532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys	
160 165 170	
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag	580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys	
175 180 185	
ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg	629
Pro Arg Arg	
190	
gaaccagatc tctcaccagg	649

<210> 2
 <211> 191
 <212> PRT
 <213> Nucleotide Sequence of VEGF165

<400> 2	
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu	
1 5 10 15	
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly	
20 25 30	

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 3
 <211> 1094
 <212> DNA
 <213> Nucleotide Sequence of SOM175

<220>
 <221> CDS
 <222> (3)..(623)

<400> 3
 cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
50 55 60
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
65 70 75
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80 85 90 95
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
100 105 110
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
115 120 125
aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac 431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His
130 135 140
cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca 479
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala
145 150 155
ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct 527
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser
160 165 170 175
gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc 575
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala
180 185 190
gct gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct 623
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
195 200 205
tagagctcaa cccagacacc tgcaggtgcc ggaagctgcg aaggtgacac atggcttttc 683
agactcagca ggggtgacttg cctcagaggc tatatcccag tgggggaaca aaggggagcc 743

tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
 ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattcttaca actggctctt 983
 cctccccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043
 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4
 <211> 207
 <212> PRT
 <213> Nucleotide Sequence of SOM175

<400> 4
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala

	165		170		175										
His	Ala	Ala	Pro	Ser	Thr	Thr	Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Ala
			180					185					190		
Ala	Ala	Ala	Asp	Ala	Ala	Ala	Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala	
		195					200					205			

<210> 5
 <211> 993
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<220>
 <221> CDS
 <222> (3)..(566)

<400> 5
 cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag . 47
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
 Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
 130 135 140
 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
 145 150 155
 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
 160 165 170 175
 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185
 cttttcagac tcagcagggt gacttgcttc agaggctata tcccagtggg ggaacaaagg 636
 ggagcctggt aaaaaacagc caagcccca agacctcagc ccaggcagaa gctgctctag 696
 gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tcctgaggg catcatcaaa 756
 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816
 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876
 gctcttcttc cctcactaa gaagacccaa acctctgcat aatgggattt gggctttggt 936
 acaagaactg tgaccccaaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993

<210> 6
 <211> 188
 <212> PRT
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
 130 135 140
 Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160
 Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180 185

<210> 7
 <211> 858
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
 <221> CDS
 <222> (3)..(431)

<400> 7
 cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95
 Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
35 40 45
cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
50 55 60
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
65 70 75
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80 85 90 95
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
100 105 110
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
115 120 125
aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg 431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140
tgacacatgg cttttcagac tcagcagggg gacttgcttc agaggctata tcccagtggg 491
ggaacaaagg ggagcctggg aaaaaacagc caagccccca agacctcagc ccaggcagaa 551
gctgctctag gacctgggcc tctcagaggg ctcttctgcc atcccttgctc tcctgagggc 611
catcatcaaa caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata 671
ccagctcagg ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat 731
cttacaactg gctcttcttc ccctcactaa gaagacccaa acctctgcat aatgggattt 791
gggcttttggg acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa 851

aaaaaaa

858

<210> 8
<211> 143
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140

<210> 9
<211> 910
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
<221> CDS
<222> (3)..(305)

<400> 9
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
1 5 10 15
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag acc taaaaaaaaag gacagtgtg tgaagccaga 335
 Gln Val Arg Met Gln Thr
 100
 cagggctgcc actccccacc accgtcccca gccccgttct gttccgggct gggactctgc 395
 ccccgagca ccctccccag ctgacatcac ccatcccact ccagccccag gccctctgc 455
 ccacgtgca cccagcacca ccagcgccct gacccccgga cctgccgctg ccgctgccga 515
 cgccgcagct tcctccgttg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575
 tgccggaagc tgcaaggtg acacatggct tttcagactc agcaggggtga cttgcctcag 635
 aggctatatc ccagtgggga acaaagagga gcctggtaaa aaacagccaa gcccccaaga 695
 cctcagccca ggcagaagct gctctaggac ctgggcctct cagaggggtc ttctgccatc 755
 ccttgctctc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815
 gcaagagggg tcacatacca gctcagggga gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaactggct ctcc

910

<210> 10
<211> 101
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Thr
100

<210> 11
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 11
accaccacct ccctgggctg gcatgtggca cgtgcataaa cg

42

<210> 12
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 12
agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13
<211> 38
<212> DNA

<213> Oligonucleotide

<400> 13

gacacctgggg ctggagtggg atggatgatg tcagctgg

38

<210> 14

<211> 40

<212> DNA

<213> Oligonucleotide

<400> 14

gcgggcagag gacacctggg ctgtctggcc tcacagcact

40

<210> 15

<211> 236

<212> DNA

<213> Human SOM175

<400> 15

atgagggggcc aggtacgtga ggtctccac agggccctgg aaagaatact tacatctgct 60

cccatggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120

ttttcaagac ctaaagacag gtgagtcttt ctctccgta ggctgcctcc agccccaggc 180

ccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16

<211> 1242

<212> DNA

<213> mVRF

<220>

<221> CDS

<222> (166)..(789)

<400> 16

gcacgagctc aggcgctgc tgcggcgctg cgttgcgctg cctgcgcca gggctcggga 60

gggggcccgc gaggagccgc cccctgcgcc ccgccccggg tccccgggtc cgcgccatgg 120

ggcgggctctg gctgaccccc cccacaccg ccgggctagg gcccg atg agc ccc ctg 177

Met Ser Pro Leu

1

ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu	Ala	Arg	Thr	Gln	
5					10					15					20	
gcc	cct	gtg	tcc	cag	ttt	gat	ggc	ccc	agt	cac	cag	aag	aaa	gtg	gtg	273
Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln	Lys	Lys	Val	Val	
				25					30					35		
cca	tgg	ata	gac	gtt	tat	gca	cgt	gcc	aca	tgc	cag	ccc	agg	gag	gtg	321
Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln	Pro	Arg	Glu	Val	
			40					45					50			
gtg	gtg	cct	ctg	agc	atg	gaa	ctc	atg	ggc	aat	gtg	gtc	aaa	caa	cta	369
Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val	Val	Lys	Gln	Leu	
		55					60					65				
gtg	ccc	agc	tgt	gtg	act	gtg	cag	cgc	tgt	ggc	ggc	tgc	tgc	cct	gac	417
Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	Cys	Cys	Pro	Asp	
	70					75					80					
gat	ggc	ctg	gaa	tgt	gtg	ccc	act	ggg	caa	cac	caa	gtc	cga	atg	cag	465
Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	Val	Arg	Met	Gln	
85					90					95					100	
atc	ctc	atg	atc	cag	tac	ccg	agc	agt	cag	ctg	ggg	gag	atg	tcc	ctg	513
Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	Glu	Met	Ser	Leu	
				105					110					115		
gga	gaa	cac	agc	caa	tgt	gaa	tgc	aga	cct	aaa	aaa	aag	gag	agt	gct	561
Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Lys	Glu	Ser	Ala	
			120					125					130			
gtg	agg	cca	gac	agg	gtt	gcc	ata	ccc	cac	cac	cgt	ccc	cag	ccc	cgc	609
Val	Arg	Pro	Asp	Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	
		135				140						145				
tct	gtt	ccg	ggc	tgg	gac	tct	acc	ccg	gga	gca	ccc	tcc	cca	gct	gac	657
Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	
	150					155					160					
atc	atc	cat	ccc	act	cca	gcc	cca	gga	tcc	tct	gcc	cgc	ctt	gca	ccc	705
Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	
165					170					175					180	
agc	gcc	gcc	aac	gcc	ctg	acc	ccc	gga	cct	gcc	gtt	gcc	gct	gta	gac	753
Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val	Ala	Ala	Val	Asp	

185 190 195
 gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc 799
 Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
 200 205
 agacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacgggc 859
 ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacctcct 919
 cagtctggga ggtcactgcc ccaggacctg gaccttttag agagctctct cgccatcttt 979
 tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctgagggggc 1039
 aggggtactct ctcaactaac caccctgggc aagtgagcat cttctggctg gctgtctccc 1099
 ctcaactatga aaaccccaaa cttctaccaa taacgggatt tgggttctgt tatgataact 1159
 gtgacacaca cacacactca cactctgata aaagagatgg agacactaaa aaaaaaaaaa 1219
 aaaaaaaaaa aaaaaaaaaa aaa 1242

<210> 17
 <211> 207
 <212> PRT
 <213> mVRF

<400> 17
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
 20 25 30
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
 50 55 60
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
 130 135 140

Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro
145					150					155					160
Ser	Pro	Ala	Asp	Ile	Ile	His	Pro	Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala
				165					170					175	
Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn	Ala	Leu	Thr	Pro	Gly	Pro	Ala	Val
			180					185					190		
Ala	Ala	Val	Asp	Ala	Ala	Ala	Ser	Ile	Ala	Lys	Gly	Gly	Ala		
		195					200				205				

<210> 18
 <211> 188
 <212> PRT
 <213> mVRF167

<400> 18

Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Val	Ala	Leu	Leu	Gln	Leu
1				5					10					15	
Ala	Arg	Thr	Gln	Ala	Pro	Val	Ser	Gln	Phe	Asp	Gly	Pro	Ser	His	Gln
			20					25					30		
Lys	Lys	Val	Val	Pro	Trp	Ile	Asp	Val	Tyr	Ala	Arg	Ala	Thr	Cys	Gln
		35					40					45			
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Ser	Met	Glu	Leu	Met	Gly	Asn	Val
	50					55					60				
Val	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly
	65				70					75					80
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln
				85					90					95	
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Gln	Tyr	Pro	Ser	Ser	Gln	Leu	Gly
			100					105					110		
Glu	Met	Ser	Leu	Gly	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys
		115					120					125			
Lys	Glu	Ser	Ala	Val	Arg	Pro	Asp	Ser	Pro	Arg	Ile	Leu	Cys	Pro	Pro
	130					135					140				
Cys	Thr	Gln	Arg	Arg	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg
145					150					155					160
Cys	Arg	Arg	Arg	Arg	Phe	Leu	His	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu
				165					170					175	
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Pro	Arg	Lys				
			180					185							

<210> 19
 <211> 188

<212> PRT
<213> hVRF167

<400> 19

Met	Ser	Pro	Leu	Leu	Arg	Arg	Leu	Leu	Leu	Ala	Ala	Leu	Leu	Gln	Leu	
1				5					10					15		
Ala	Pro	Ala	Gln	Ala	Pro	Val	Ser	Gln	Pro	Asp	Ala	Pro	Gly	His	Gln	
			20					25					30			
Arg	Lys	Val	Val	Ser	Trp	Ile	Asp	Val	Tyr	Thr	Arg	Ala	Thr	Cys	Gln	
		35					40					45				
Pro	Arg	Glu	Val	Val	Val	Pro	Leu	Thr	Val	Glu	Leu	Met	Gly	Thr	Val	
	50					55					60					
Ala	Lys	Gln	Leu	Val	Pro	Ser	Cys	Val	Thr	Val	Gln	Arg	Cys	Gly	Gly	
65					70					75					80	
Cys	Cys	Pro	Asp	Asp	Gly	Leu	Glu	Cys	Val	Pro	Thr	Gly	Gln	His	Gln	
				85					90					95		
Val	Arg	Met	Gln	Ile	Leu	Met	Ile	Arg	Tyr	Pro	Ser	Ser	Gln	Leu	Gly	
			100					105					110			
Glu	Met	Ser	Leu	Glu	Glu	His	Ser	Gln	Cys	Glu	Cys	Arg	Pro	Lys	Lys	
		115					120					125				
Lys	Asp	Ser	Ala	Val	Lys	Pro	Asp	Ser	Pro	Arg	Pro	Leu	Cys	Pro	Arg	
	130					135					140					
Cys	Thr	Gln	His	His	Gln	Arg	Pro	Asp	Pro	Arg	Thr	Cys	Arg	Cys	Arg	
145					150				155						160	
Cys	Arg	Arg	Arg	Ser	Phe	Leu	Arg	Cys	Gln	Gly	Arg	Gly	Leu	Glu	Leu	
				165					170					175		
Asn	Pro	Asp	Thr	Cys	Arg	Cys	Arg	Lys	Leu	Arg	Arg					
			180					185								

<210> 20
<211> 71
<212> PRT
<213> mVRF186

<400> 20

Arg	Val	Ala	Ile	Pro	His	His	Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro	Gly	
1				5					10					15		
Trp	Asp	Ser	Thr	Pro	Gly	Ala	Pro	Ser	Pro	Ala	Asp	Ile	Ile	His	Pro	
			20					25					30			
Thr	Pro	Ala	Pro	Gly	Ser	Ser	Ala	Arg	Leu	Ala	Pro	Ser	Ala	Ala	Asn	
		35					40					45				

Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp Ala Ala Ala Ser
50 55 60

Ser Ile Ala Lys Gly Gly Ala
65 70

<210> 21
<211> 71
<212> PRT
<213> hVRF186

<400> 21
Arg Ala Ala Thr Pro His His Arg Pro Gln Pro Arg Ser Val Pro Gly
1 5 10 15

Trp Asp Ser Ala Pro Gly Ala Pro Ser Pro Ala Asp Ile Thr His Pro
20 25 30

Thr Pro Ala Pro Gly Pro Ser Ala His Ala Ala Pro Ser Thr Thr Ser
35 40 45

Ala Leu Thr Pro Gly Pro Ala Ala Ala Ala Asp Ala Ala Ala Ser
50 55 60

Ser Val Ala Lys Gly Gly Ala
65 70

<210> 22
<211> 214
<212> PRT
<213> mVEGF188

<400> 22
Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly
20 25 30

Glu Gln Lys Ser His Glu Val Ile Lys Phe Met Asp Val Tyr Gln Arg
35 40 45

Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr
50 55 60

Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
65 70 75 80

Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr
85 90 95

Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
100 105 110

Ser	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Ser	Arg	Cys	Glu
		115					120					125			
Cys	Arg	Pro	Lys	Lys	Asp	Arg	Thr	Lys	Pro	Glu	Lys	Lys	Ser	Val	Arg
	130					135					140				
Gly	Lys	Gly	Lys	Gly	Gln	Lys	Arg	Lys	Arg	Lys	Lys	Ser	Arg	Phe	Lys
145					150					155					160
Ser	Trp	Ser	Val	His	Cys	Glu	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu
				165					170					175	
Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp
			180					185					190		
Ser	Arg	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg
		195					200					205			
Cys	Asp	Lys	Pro	Arg	Arg										
	210														